On page 47, line 15, please replace "Felix" with -- FELIX--, and "nmrPipe" with -- NMRPIPE--.

On page 49, line 21, please replace "Quanta" with -- QUANTA--.

On page 53, line 29, please replace "Hi-Trap" with --HI-TRAP--.

On page 54, line 3, please replace "ResourceS" with --RESOURCES®--.

On page 57, line 24, please replace "NMRPipe" with --NMRPIPE--, and at line 25 please replace "NMRView" with --NMRVIEW--.

On page 12, please replace lines 7-12 with the following text:

--**Figure 1A**. β-Strand and loop topology of anti-lysozyme immunoglobulin D1.3. (Bhat et al., 1994) The locations of complementarity determining regions (CDRs, hypervariable regions) are indicated.

Figure 1B. β-Strand and loop topology of the10th type III domain of human fibronectin. (Main et al., 1992) The locations of the integrin-binding Arg-Gly-Asp (RGD) sequence is indicated.

Figure 1C. MOLSCRIPT representation of anti-lysozyme immunoglobulin D1.3. (Kraulis, 1991; Bhat et al., 1994) The locations of complementarity determining regions (CDRs, hypervariable regions) are indicated.

Figure 1D. MOLSCRIPT representation of the10th type III domain of human fibronectin. (Kraulis, 1991; Main et al., 1992) The locations of the integrin-binding Arg-Gly-Asp (RGD) sequence is indicated.--

On page 12, please replace lines 20-22 with the following text:

--**Figure 3A**. Far UV CD spectra of wild-type Fn3 at 25°C and 90°C. Fn3 (50 μM) was dissolved in sodium acetate (50 mM, pH 4.6).

Figure 3B. Thermal denaturation of Fn3 monitored at 215 nm. Temperature was increased at a rate of 1°C/min.--

Please replace the text on page 12, line 23 to page 13, line 4 with the following text:

--**Figure 4A.** Cα trace of the crystal structure of the complex of lysozyme (HEL) and the Fv fragment of the anti-hen egg-white lysozyme (anti-HEL) antibody D1.3 (Bhat et al., 1994). Side chains of the residues 99-102 of VH CDR3, which make contact with HEL, are also shown.

Figure 4B. Contact surface area for each residue of the D1.3 VH-HEL and VH-VL interactions plotted vs. residue number of D1.3 VH. Surface area and secondary structure were determined using the program DSSP (Kabsh and Sander, 1983).

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Figure 4C. Schematic drawings of the β-sheet structure of the F strand-loop-G strand moieties of D1.3 VH. The boxes denote residues in β-strands and ovals those not in strands. The shaded boxes indicate residues of which side chains are significantly buried. The broken lines indicate hydrogen bonds.

Figure 4D. Schematic drawings of the β-sheet structure of the F strand-loop-G strand moieties of Fn3. The boxes denote residues in β-strands and ovals those not in strands. The shaded boxes indicate residues of which side chains are significantly buried. The broken lines indicate hydrogen bonds.--

Please replace the text on page 14, lines13-23 with the following text:

Figure 15A. Characterization of the binding reaction of Ubi4-Fn3 to the target, ubiquitin. Phage ELISA analysis of binding of Ubi4-Fn3 to ubiquitin. The binding of Ubi4-phages to ubiquitin-coated wells was measured. The control experiment was performed with wells containing no ubiquitin.

B5

Figure 15B. Competition phage ELISA of Ubi4-Fn3. Ubi4-Fn3-phages were preincubated with soluble ubiquitin at an indicated concentration, followed by the phage ELISA detection in ubiquitin-coated wells.

Figure 15C. Competition phage ELISA testing the specificity of the Ubi4 clone. The Ubi4 phages were preincubated with 250 μg/ml of soluble proteins, followed by phage ELISA as in (b).

Figure 15D. ELISA using free proteins.--